RESEARCHER DEVELOPMENT

Clustering
(unsupervised learning)

John Joseph Valletta

University of Exeter, Penryn Campus, UK

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www.exeter.ac.uk/as/rdp/

Overview

- What is clustering?
- Major types of clustering methods
- k-means clustering
- Agglomerative hierarchical clustering
- Gaussian mixture models
- How do we determine the correct number of clusters?

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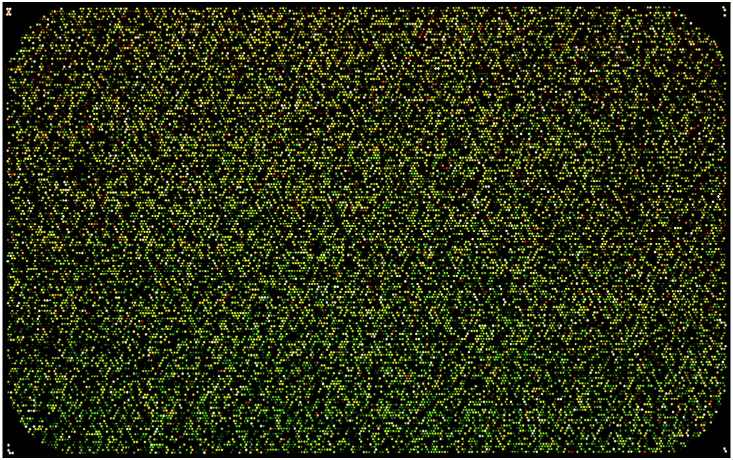
What's the problem?

Well, it's driven by your data, e.g which of these genes are co-regulated?



We want to find some underlying structure in the data → **Clustering**

What's the problem?

Gene expression:	discovering co-regulated genes
Biological systematics:	finding organisms sharing similar attributes
Computer vision:	segmenting a digital image for object recognition
Epidemiology:	identifying geographical clusters of diseases
Medical imaging:	differentiating between tissues
Mathematical chemistry:	grouping compounds by topological indices

Clustering is particularly useful in applications where labelling the data is very time consuming/expensive

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Formal definition

Identifying homogeneous and well separated groups of data points (features) by some similarity measure

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Informal definition

The process of stereotyping your data
e.g *these* are round(ish) faces, *these* are short(ish) people

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But how many groups?

An unsolved problem. Issue lies in the subjectivity of the word **similar** and its mathematical definition

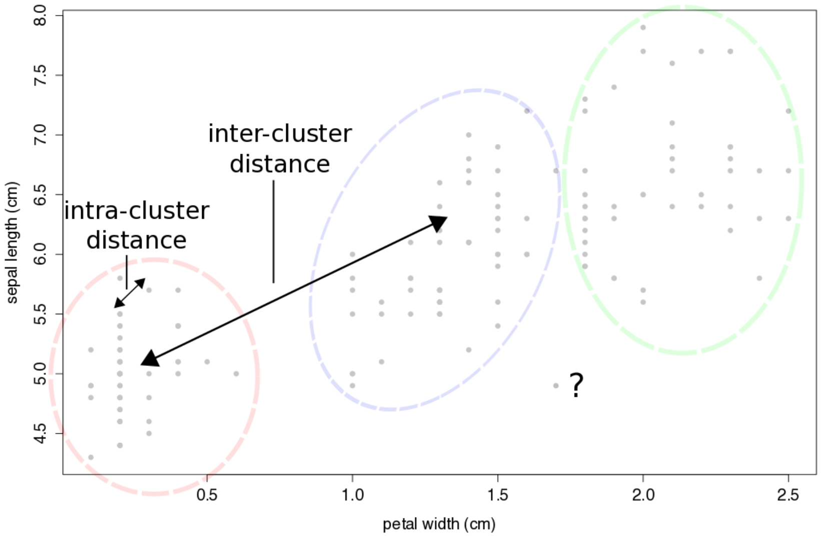
Are they similar?

Are they similar?

What are we after?

Motivation: How is the data structured? Any outliers?

Goals: *High* intra-cluster similarity and *low* inter-cluster similarity



Major types of clustering methods

Partitional: The data (feature) space is partitioned into k regions

Hierarchical: Iteratively merging small clusters into larger ones (*agglomerative*) or breaking large clusters into smaller ones (*divisive*)

Distribution-based: Fit k multivariate statistical distributions

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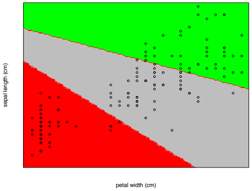

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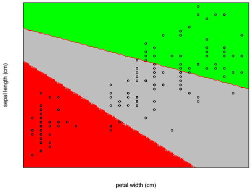

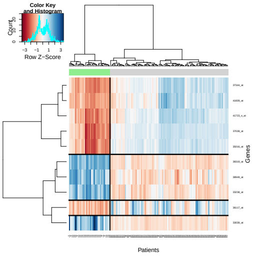

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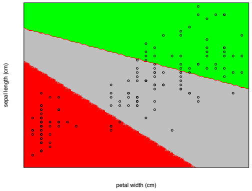

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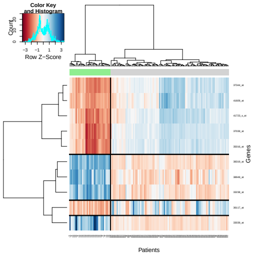
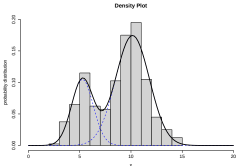
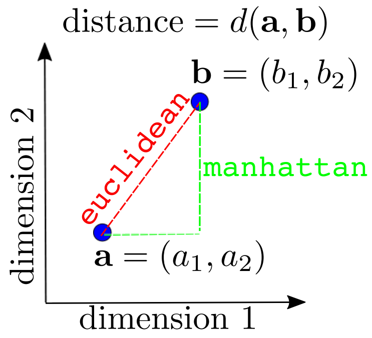


Distribution-based: Fit k multivariate statistical distributions



Similarity measures

- A *distance* metric quantifies how *close* two data points are
- Several ways to define this distance which has a direct impact on the clustering result



$\text{distance} = d(\mathbf{a}, \mathbf{b})$
$\mathbf{b} = (b_1, b_2)$
euclidean
manhattan
$\mathbf{a} = (a_1, a_2)$
dimension 2
dimension 1

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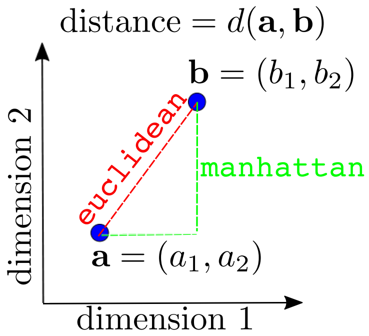
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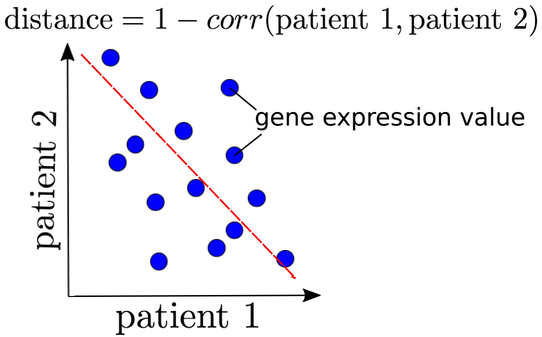
$\text{distance} = 1 - corr(\text{patient 1}, \text{patient 2})$
gene expression value
patient 2
patient 1

k-means clustering

```
fit <- kmeans(x, centers)
# x - numeric matrix of data
# centers - no. of clusters k
```

1. Select k centroids at random
2. Calculate distance between centroids and each data point
3. Assign each data point to the closest centroid
4. Compute new centroids; the average of all data points in that cluster
5. Repeat steps 2 to 4 until data points remain in the same cluster or some maximum number of iterations reached

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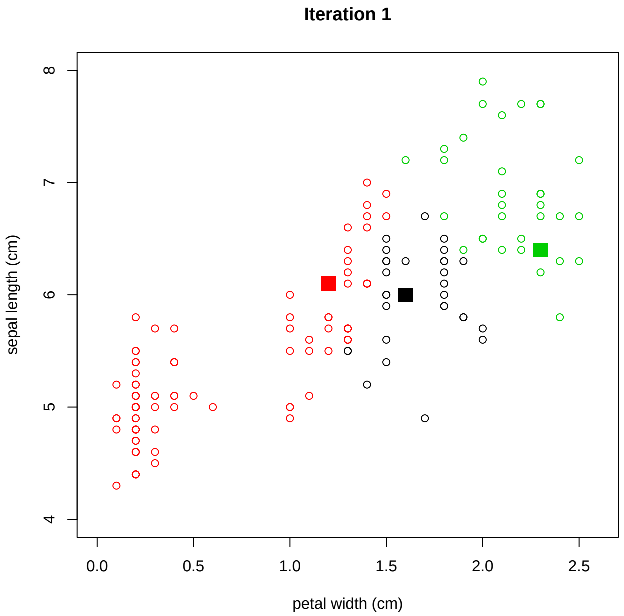
Note: k-means clustering should *only* be used with continuous data

k-means clustering



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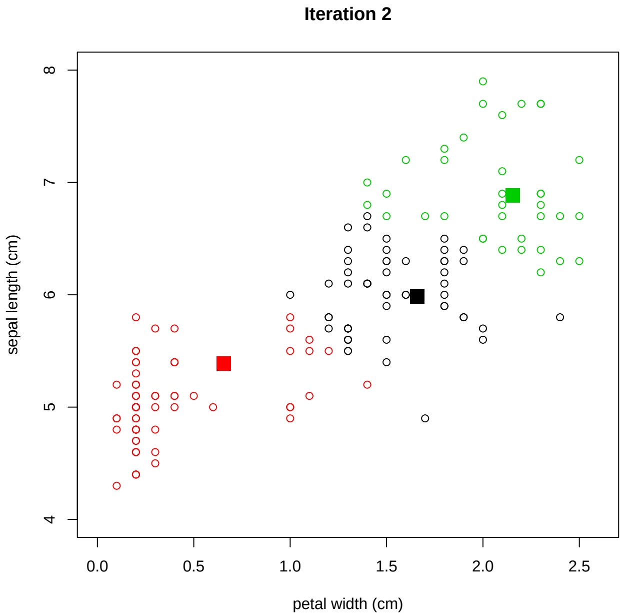

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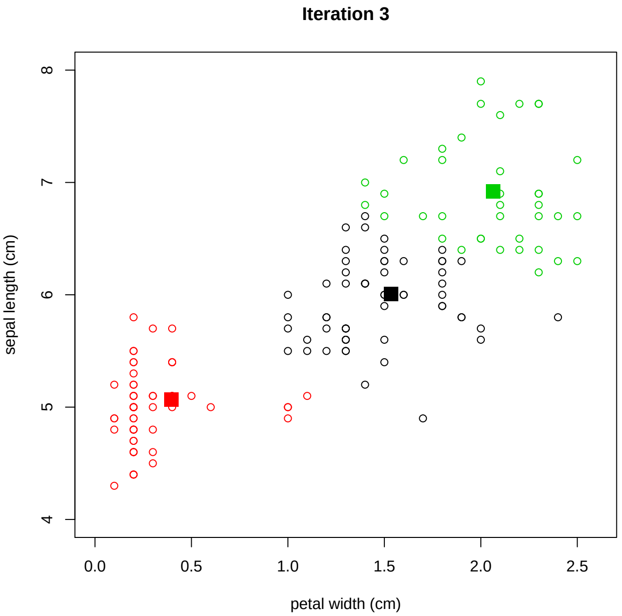

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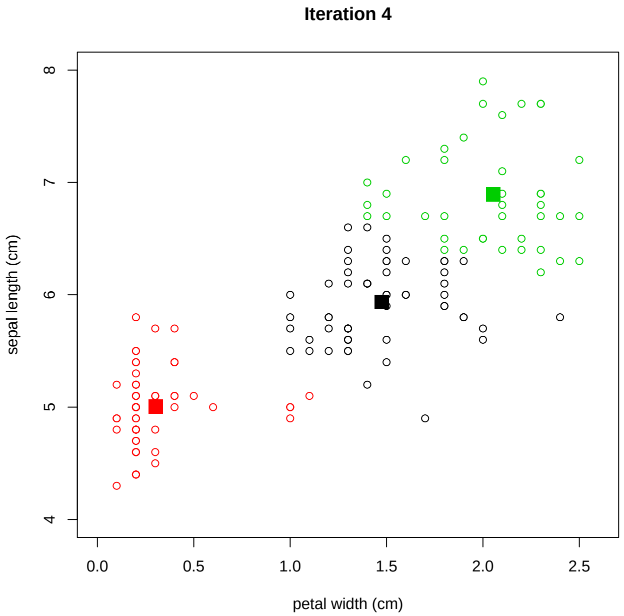

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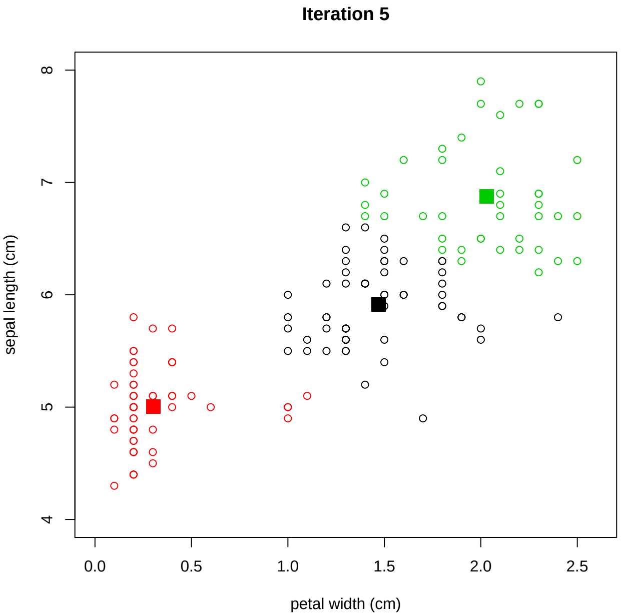

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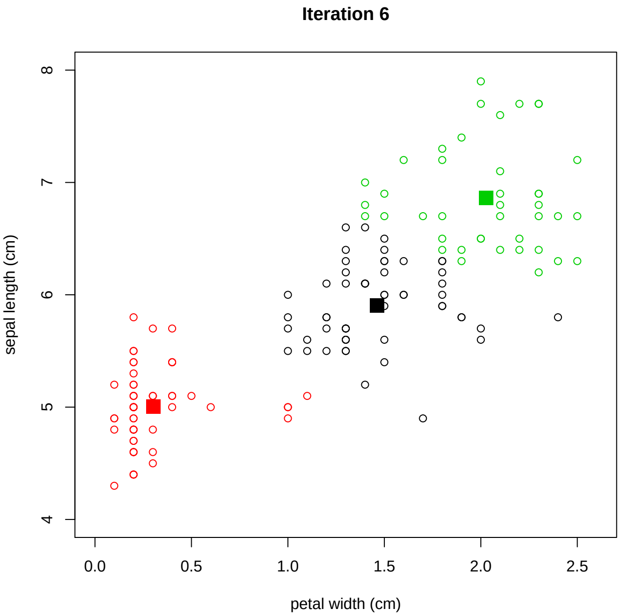

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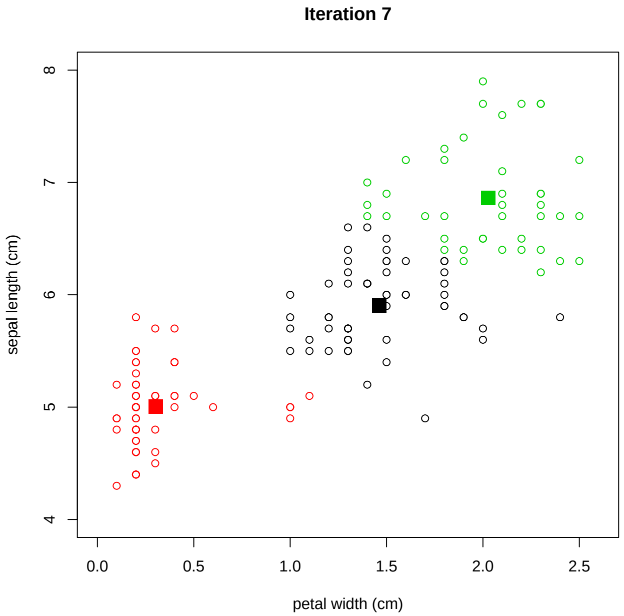

k-means clustering

Pros

- Simple and intuitive
- Computationally inexpensive/fast

Cons

- What is k?
- Only applicable to continuous data where a mean is defined
- No guarantee of a global optimum solution

Agglomerative hierarchical clustering

```
d <- dist(as.matrix(data), method)
# data - data frame
# method - distance method e.g "euclidean" or "manhattan"
fit <- hclust(d, method)
# method - linkage function e.g "complete" or "single"
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1. Assign each data point as its own cluster
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Note: Step 3 is *key*, the distance method and linkage function dictate the final result

Hierarchical clustering: Link method

How do we compute the inter-cluster distance? The *linkage function*

Centroid: mean of data points (same as in k-means)

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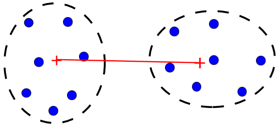

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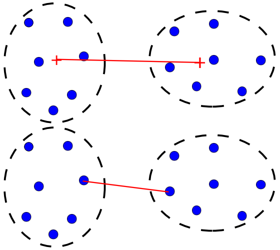

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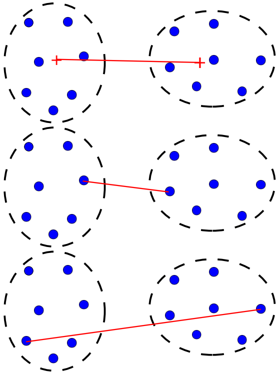

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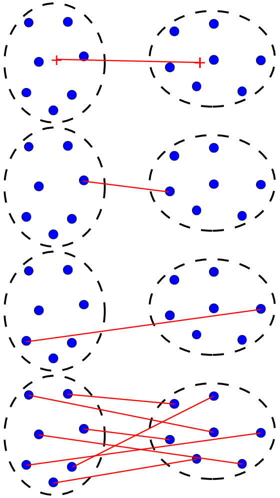
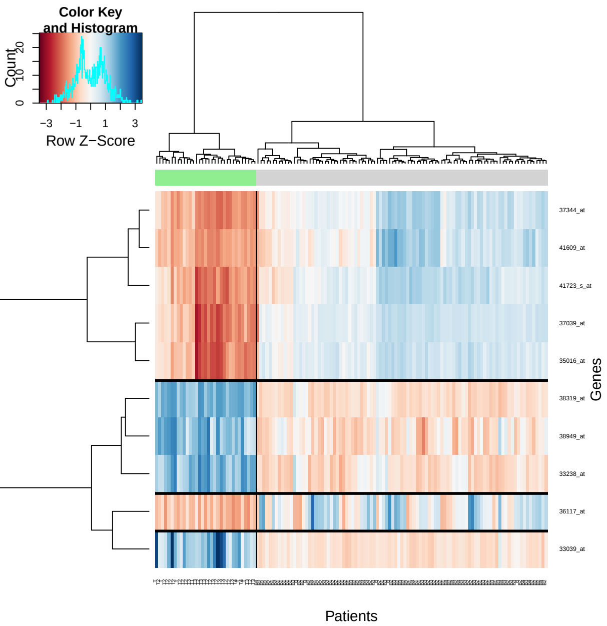


Hierarchical clustering in gene expression studies



Hierarchical clustering

Pros

- No need to specify k
- Results can be visualised nicely irrespective of number of dimensions

Cons

- Can be computationally expensive
- Interpretation is subjective. Where should we draw the line (to separate clusters)?
- Choice of distance method and linkage function can significantly change the result

Gaussian mixture models

```r
library(mclust)
fit <- Mclust(data, G)
# data - data frame
# G - no. of Gaussians
```

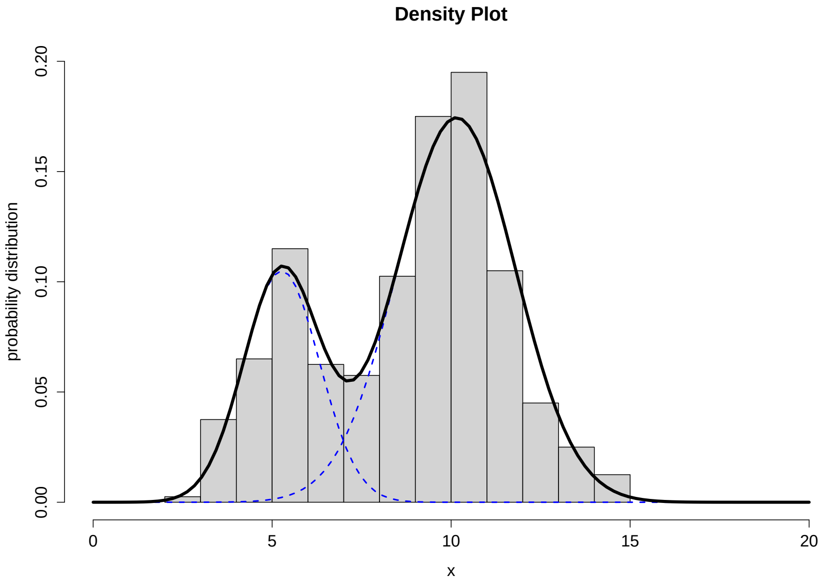
1. Fit k multivariate Gaussian distributions

The Expectation-Maximisation (EM) algorithm is used to estimate the parameters π_i (mixing coefficients), μ_i and σ_i

$$p(x) = \sum_{i=1}^{k} \pi_i \mathcal{N}(x|\mu_i, \Sigma_i) \text{ and } \sum_{i=1}^{k} \pi_i = 1$$

Can be seen as a "soft" version of k-means because *every* point is part of *every* cluster but with varying levels of membership

Gaussian mixture models



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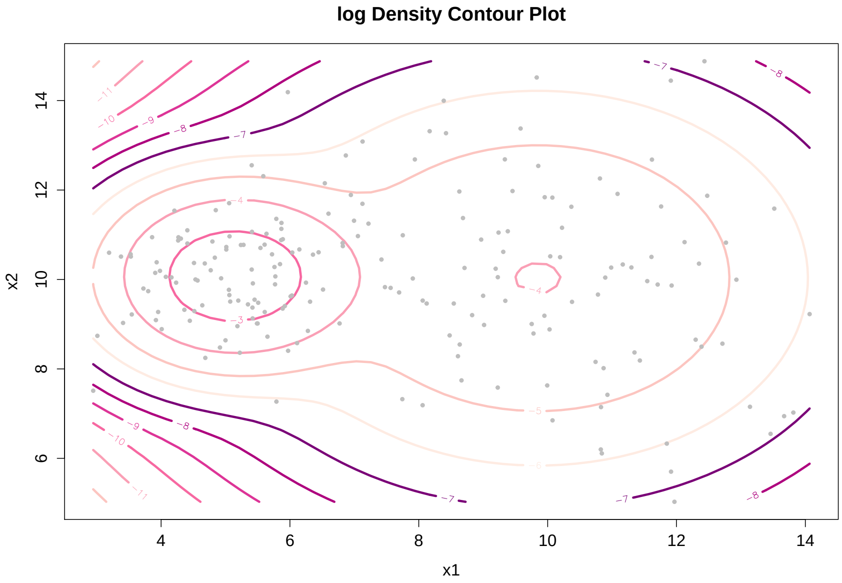

Gaussian mixture models

Pros

- Intuitive interpretation
- Computationally inexpensive

Cons

- What is k?
- Strong assumption on the data (normality)
- No guarantee of a global optimum solution

How do we determine the correct number of clusters?

Short answer: you can't

Because data is unlabelled the correct number of k is ambiguous

However we can plot some indices as a function of k to help us evaluate cluster validity:

- Within and between clusters sum-of-squares distances
- Akaike Information Criterion (AIC) or Bayesian Information Criterion (BIC) when using distribution-based methods
- Silhouette plot

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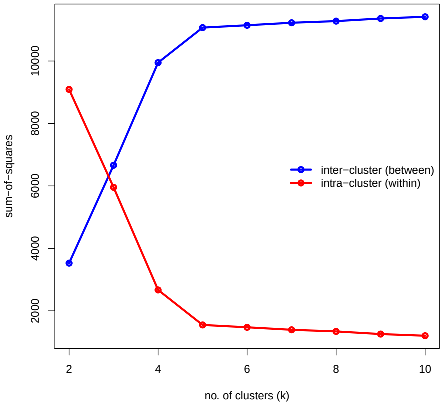

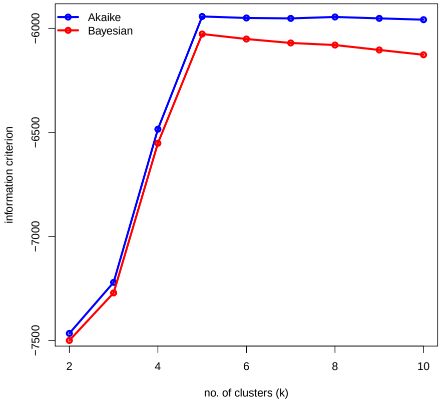

How do we determine the correct number of clusters?

The `NbClust` package provides 30 different cluster validity metrics. A majority vote can be taken to deduce the appropriate number of clusters

```
library(NbClust)
NbClust(data, distance, method, min.nc, max.nc, index)
# data - data frame
# distance - similarity measure e.g "euclidean"
# method - clustering algorithm e.g "kmeans"
# min.nc - min number of clusters to consider
# max.nc - max number of clusters to consider
# index - which indices to compute, "all" computes all of them
```

Note:

- Indices *only* give us a ballpark range for "correct" number of clusters
- Are they biologically relevant? Prior knowledge to the rescue
- E.g how many different phenotypes are you expecting?